

10/566851

## SEQUENCE LISTING

JAP20 Rec'd PCT/PTO 01 FEB 2006

<110> Jacquemin, Marc  
Saint-Remy, Jean-Marie

<120> Variable antibodies

<130> 50304/112001

<150> GB 0319118.6

<151> 2003-08-14

<150> GB 0319345.5

<151> 2003-08-18

<160> 32

&lt;170&gt; PatentIn version 3.3

 $\langle 210 \rangle$  1

<211> 496

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<213> Homo sapiens

$\langle 220 \rangle$

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<222> (1) .. (495)

<223> KRIX-1 heavy chain variable region

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1 5 10 15

gcc cac tcc cag gtg caa ctg gtg caa tct ggg gct gag gtg aag aag 96  
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

	20	25	30	
cct ggg gcc tca gtg aag gtc tcc tgc aag acc tct gga tac aac ttc				144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe				
	35	40	45	
acc ggc tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac				192
Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His				
	50	55	60	
tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc				240
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile				
	65	70	75	80
aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg				288
Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg				
	85	90	95	
gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg				336
Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu				
	100	105	110	
agc agg ctg aca tct gac gac acg gcc atg tat tac tgt gcg aga gcc				384
Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala				
	115	120	125	
gac aac tat ttc gat att gtg act ggc tat act tct cat tac ttt gac				432
Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp				
	130	135	140	
tac tgg ggc cgg gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag				480
Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys				
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Gly Pro Ser Val Phe				
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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe			
35	40	45	

Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His  
50 55 60

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile  
65 70 75 80

Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg  
85 90 95

Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu  
100 105 110

Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala  
115 120 125

Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp  
130 135 140

Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
145 150 155 160

Gly Pro Ser Val Phe  
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<222> (1)..(429)  
<223> KRIX-1 light chain variable region

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<223> nucleotide sequence encoding CDR2

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1 5 10 15	

gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct	96
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser	
20 25 30	

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt	144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser	
35 40 45	

gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct	192
Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala	
50 55 60	

ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca	240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro	
65 70 75 80	

cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc	288
His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	
85 90 95	

agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat	336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr	
100 105 110	

ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc	384
Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	
115 120 125	

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct	429
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser	
130 135 140	

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser

20

25

30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
 35 40 45

Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
 50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro  
 65 70 75 80

His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
 85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr  
 100 105 110

Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
 130 135 140

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<400> 5  
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<210> 6  
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<400> 6  
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gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct	96
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser	
20 25 30	
ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt	144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct	192
Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala	
50 55 60	
ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca	240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro	
65 70 75 80	
cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc	288
His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	
85 90 95	
agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat	336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr	
100 105 110	
ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc	384
Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	
115 120 125	
aaa cga ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga	432
Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
130 135 140	
tcg cag gta cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg	480
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly	
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gcc tca gtg aag gtc tcc tgc aag acc tct gga tac caa ttc acc ggc	528
Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly	
165 170 175	
tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac tgg gtg	576
Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val	
180 185 190	
cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc aac cct	624
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro	
195 200 205	
aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg gtc acc	672
Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr	
210 215 220	
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Met	Ser	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Arg		
225					230					235					240		
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Leu	Thr	Ser	Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Arg	Ala	Asp	Asn		
				245					250					255			
tat	ttc	gat	att	gtg	act	ggc	tat	act	tct	cat	tac	ttt	gac	tac	tgg		816
Tyr	Phe	Asp	Ile	Val	Thr	Gly	Tyr	Thr	Ser	His	Tyr	Phe	Asp	Tyr	Trp		
			260					265					270				
ggc	cgg	gga	acc	ctg	gtc	acc	gtc	tcc	tca	cat	cat	cat	cat	cat	cat		864
Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	His	His	His	His	His	His		
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tga																	867

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			20					25					30				

Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser		
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Val	Ala	Ser	Ala	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala		
	50					55					60						

Pro	Arg	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Asp	Ile	Pro		
65				70						75				80			

His	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile		
			85					90					95				

Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr		
		100						105					110				

Gly	Thr	Ser	Ala	Leu	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile		
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115	120	125
Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly		
130	135	140
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly		
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Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly		
165	170	175
Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val		
180	185	190
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro		
195	200	205
Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr		
210	215	220
Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg		
225	230	235
Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn		
245	250	255
Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp Tyr Trp		
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Gly Arg Gly Thr Leu Val Thr Val Ser Ser His His His His His His		
275	280	285

<210> 27  
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<222> (352)..(384)
<223> nucleotide sequence encoding CDR3

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1 5 10 15

gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

ccc ggg tcg tcg gtg atg gtc tcc tgc aag gct tct gga ggc acc ttc 144
Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35 40 45

agc agc ttt ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt 192
Ser Ser Phe Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

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gag tgg gtg gga ggg atc atc cct atc ttt ggt aca gca aac acc gca 240  
Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala  
65 70 75 80

aca	gcc	tac	ata	cga	ctg	agg	agc	ctg	aga	tct	gaa	gat	acg	gcc	gtg	336
Thr	Ala	Tyr	Ile	Arg	Leu	Arg	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			

gtc tgg ggc caa ggg aca atg gtc acc gtc tct tca gcc tcc acc aag 432  
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130 135 140

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Met	Asp	Trp	Thr	Trp	Arg	Phe	Leu	Phe	Val	Val	Ala	Ala	Ala	Ala	Gly
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35 40 45

Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala  
65 70 75 80

Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Val Gly Gly Arg Asp Ala Tyr Ser Phe Asp Gly Phe Asp  
115 120 125

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro  
145 150

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1 5 10 15

tcc gtg gcc tcc tct ggg ctg act cag cca cac tca gtg tcc gtg tcc 96  
Ser Val Ala Ser Ser Gly Leu Thr Gln Pro His Ser Val Ser Val Ser  
20 25 30

cca gga cag aca gcc aac atc acc tgc tct aga gat aag ttg ggt cat 144

Pro Gly Gln Thr Ala Asn Ile Thr Cys Ser Arg Asp Lys Leu Gly His  
35 40 45

aaa ttt gct tcc tgg tat caa cag aag cca ggc cag tcc cct gct ctt 192  
Lys Phe Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Ala Leu  
50 55 60

ctc atc tat caa gac agc aag cgg ccc tca ggg atc cct gag cga ttc 240  
Leu Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
65 70 75 80

tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc agc ggg acc 288  
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
85 90 95

cag gct atg gat gag gct gac tat tac tgt cag gcg tgg gac aac acc 336  
Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Asn Thr  
100 105 110

act gcc gta ttc ggc gga ggg acc aag ttg aca gtc cta agt cag ccc 384  
Thr Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro  
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aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc 420  
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser  
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<213> Homo sapiens

<400> 32

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Ser Val Ala Ser Ser Gly Leu Thr Gln Pro His Ser Val Ser Val Ser  
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Pro Gly Gln Thr Ala Asn Ile Thr Cys Ser Arg Asp Lys Leu Gly His  
35 40 45

Lys Phe Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Ala Leu  
50 55 60

Leu Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
85 90 95



Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Asn Thr  
100 105 110

Thr Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro  
115 120 125

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser  
130 135 140